

pMEV-2HA Molecule Information

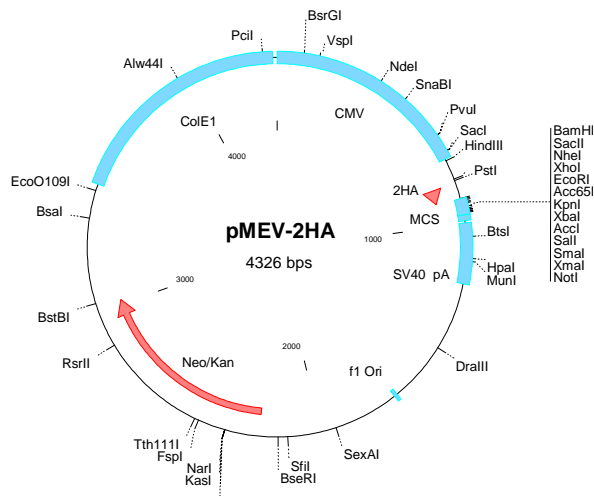
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Molecule Features:

Features	Start	End
CMV Promoter	1	750
2 x HA Coding sequence	843	902
Multiple Cloning Site (MCS)	903	964
T3 RNA Polymerase Promoter	964	985
SV40 Polyadenylation signal	993	1215
f1 Replicaiton Origin	1691	1703
Neo/Kan-Resistance Gene	2228	3022
ColE1 Replication Origin	3478	4310

Vector Map



Multiple Cloning Site Sequences

Multiple cloning site of pMEV-2HA frame A

843 *2xHA (YPYDVPDYA)*
ATGGGATACCCTTACGACGTTCTGATTACGCTTACCCTTACGACGTTCTGATTACGCT
MetGlyTyrProTyrAspValProAspTyrAlaTyrProTyrAspValProAspTyrAla

BamH I Nhe I Xho I EcoR I Kpn I Xba I Sal I Xma I Not I
GGATCCGCGGCTAGCCTCGAGAATTCACGCGTGGTACCTCTAGAGTCGACCCGGGCGGCC
GlySerAlaAlaSerLeuGluAsnSerArgValValProLeuGluSerThrArgAlaAla

—
GCTTCCCTTTAGTGAGGGTTAATGCTTC
AlaSerLeu***

Multiple cloning site of pMEV-2HA frame B

843 *2xHA (YPYDVPDYA)*
ATGGGATACCCTTACGACGTTCTGATTACGCTTACCCTTACGACGTTCTGATTACGCT
MetGlyTyrProTyrAspValProAspTyrAlaTyrProTyrAspValProAspTyrAla

BamH I Nhe I Xho I EcoR I Kpn I Xba I Sal I Xma I Not I
atGGATCCGCGGCTAGCCTCGAGAATTCACGCGTGGTACCTCTAGAGTCGACCCGGGCGGC
MetAspProArgLeuAlaSerArgIleHisAlaTrpTyrLeu***

—
CCGCTTCCCTTTAGTGAGGGTTAATGCTTC

Multiple cloning site of pMEV-2HA frame C

843 *2xHA (YPYDVPDYA)*
ATGGGATACCCTTACGACGTTCTGATTACGCTTACCCTTACGACGTTCTGATTACGCT
MetGlyTyrProTyrAspValProAspTyrAlaTyrProTyrAspValProAspTyrAla

BamH I Xho I EcoR I Kpn I Xba I Sal I Xma I Not I
tGGATCCGCGGCAAGCCTCGAGAATTCACGCGTGGTACCTCTAGAGTCGACCCGGGCGGCCG
TrpIleArgGlyLysProArgGluPheThrArgGlyThrSerArgValAspProGlyGlyArg

TTCCCTTTAGTGAGGGTTAATGCTTC
PheProLeuValArgValAsnAla

Note: Nucleotides 903-904 (*a* and *t* in lower cases before *BamHI*) are inserted in frame B to adjust the reading frame.

Nucleotide Sequence of pMEV-2HA

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1   TCAATATTGG CCATTAGCCA TATTATTCAT TGGTTATATA GCATAAATCA ATATTGGCTA
61  TTGGCCATTG CATACGTTGT ATCTATATCA TAATATGTAC ATTTATATTG GCTCATGTCC
121 AATATGACCG CCATGTTGGC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG
181 GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC
241 GCCTGGCTGA CCGCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
301 AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC
361 CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG CCCCTATTG ACGTCAATGA
421 CGGTAAATGG CCCGCTGGC ATTATGCCCA GTACATGACC TTACGGGACT TTCCTACTTG
481 GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAC
541 CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT
601 CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAATGTC GTAACAAC TG
661 CGATCGCCCC CCCCGTTGAC GCAAATGGGC GGTAGGCGTG TACGGTGGGA GGTCTATATA
721 AGCAGAGCTC GTTTAGTGAA CCGTCAGATC ACTAGAAGCT TTATTGCGGT AGTTTATCAC
781 AGTTAAATTG CTAACGCAGT CAGTGCTTCT GACACAACAG TCTCGAECTT AAGCTGCAGA
841 CCATGGGATA CCCTTACGAC GTTCCTGATT ACGCTTACCC TTACGACGTT CCTGATTACG
901 CTGGATCCGC GGCTAGCCTC GAGAATTCAC GCGTGGTACC TCTAGAGTCG ACCCGGGCGG
961 CCGCTTCCCT TTAGTGAGGG TTAATGCTTC GAGCAGACAT GATAAGATAC ATTGATGAGT
1021 TTGGACAAAC CACAAC TAGA ATGCAGTGAA AAAAATGCTT TATTTGTGAA ATTTGTGATG
1081 CTATTGCTTT ATTTGTAACC ATTATAAGCT GCAATAAACA AGTTAACAAC AACAATTGCA
1141 TTCATTTTAT GTTTCAGGTT CAGGGGGAGA TGTGGGAGGT TTTTAAAGC AAGTAAACC
1201 TCTACAAATG TGGTAAAATC CGATAAGGAT CGATCCGGGC TACGCGTAAA TTGTAAGCGT
1261 TAATATTTTG TTAATAATTCG CGTTAAATTT TTGTTAAATC AGCTCATTTT TTAACCAATA
1321 GGCCGAAATC GGCAAATCC CTTATAAATC AAAAGAATAG ACCGAGATAG GGTGAGTGT
1381 TGTTCCAGTT TGGAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG TCAAAGGGCG
1441 AAAAACCGTC TATCAGGGCG ATGGCCCACT ACGTGAACCA TCACCCTAAT CAAGTTTTTT
1501 GGGGTCGAGG TGCCGTAAAG CACTAAATCG GAACCCTAAA GGGAGCCCC GATTTAGAGC
1561 TTGACGGGGA AAGCCGGCGA ACGTGGCGAG AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG
1621 CGTAGGGCG CTGGCAAGTG TAGCGGTCAC GCTGCGCGTA ACCACCACAC CCGCCGCGCT
1681 TAATGCGCCG CTACAGGGCG CGTCAGGTGG CACTTTTCGG GGAAATGTGC GCGGAACCCC
1741 TATTTGTTTTA TTTTCTAAA TACATTCAA TATGTATCCG CTCATGAGAC AATAACCCTG
1801 ATAAATGCTT CAATAATATT GAAAAAGGAA GAGTCCTGAG GCGGAAAGAA CCAGCTGTGG
1861 AATGTGTGTC AGTTAGGGTG TGGAAAGTCC CCAGGCTCCC CAGCAGGCAG AAGTATGCAA
1921 AGCATGCATC TCAATTAGT AGCAACCAGG TGTGGAAAGT CCCAGGCTC CCCATGAGC
1981 AGAAGTATGC AAAGCATGCA TCTCAATTAG TCAGCAACCA TAGTCCC GCCCTAACTCCG
2041 CCCATCCCGC CCCTAACTCC GCCCAGTTCC GCCCATTCTC CGCCCCATGG CTGACTAATT
2101 TTTTTTATTT ATGCAGAGGC CGAGGCCGCC TCGGCCTCTG AGCTATTCCA GAAGTAGTGA
2161 GGAGGCTTTT TTGGAGGCCT AGGCTTTTGC AAAGATCGAT CAAGAGACAG GATGAGGATC
2221 GTTTCGCATG ATTGAACAAG ATGGATTGCA CGCAGGTTCT CCGGCCGCTT GGGTGGAGAG
2281 GCTATTTCGGC TATGACTGGG CACAACAGAC AATCGGCTGC TCTGATGCCG CCGTGTTCGG
2341 GCTGTCAGCG CAGGGGCGCC CGGTTCTTTT TGTCAAGACC GACCTGTCCG GTGCCCTGAA
2401 TGAAGTCAA GACGAGGCAG CGCGGCTATC GTGGCTGGCC ACGACGGGCG TTCCTTGCGC
2461 AGCTGTGCTC GACGTTGTCA CTGAAGCGGG AAGGGACTGG CTGCTATTGG GCGAAGTGCC
2521 GGGGCAGGAT CTCCTGTCAT CTCACCTTGC TCCTGCCGAG AAAGTATCCA TCATGGCTGA
2581 TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTGACCC ACCAAGCGAA
2641 ACATCGCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTGATC AGGATGATCT
2701 GGACGAAGAG CATCAGGGGC TCGCGCCAGC CGAACTGTTT GCCAGGCTCA AGGCGAGCAT
2761 GCCCGACGGC GAGGATCTCG TCGTGACCCA TGGCGATGCC TGCTTGCCGA ATATCATGGT
2821 GGAAAATGGC CGCTTTTCTG GATTTCATCGA CTGTGGCCGG CTGGGTGTGG CGGACCGCTA
2881 TCAGGACATA GCGTTGGCTA CCCGTGATAT TGCTGAAGAG CTTGGCGGGC AATGGGCTGA
2941 CCGCTTCTC GTGCTTTACG GTATCGCCCG TCCCATTCTC CAGCGCATCG CCTTCTATCG
3001 CCTTCTTGAC GAGTTCTTCT GATCGGGACT CTGGGGTTCT AAATGACCGA CCAAGCGAGC
3061 CCCAACCTGC CATCACGAGA TTTTCGATTCC ACCGCCCTCT TCTATGAAAG CTTGGGCTTC
3121 GGAATCGTTT TCCGGGACGC CGGCTGGATG ATCCTCCAGC GCGGGGATCT CATGCTGGAG
3181 TTCTTCGCCC ACCCTAGGGG GAGGCTAACT GAAACACGGA AGGAGACAAT ACCGGAAGGA
3241 ACCCGCGCTA TGACGGCAAT AAAAAGACAG AATAAAACGC ACGGTGTTGG GTCGTTTTGT
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3301  CATAAACGCG GGGTTCGGTC CCAGGGCTGG CACTCTGTCG ATACCCCACC GAGACCCCAT
3361  TGGGGCCAAT ACGCCCGCGT TTCTTCCTTT TCCCCACCCC ACCCCCCAAG TTCGGGTGAA
3421  GGCCCAGGGC TCGCAGCCAA CGTCGGGGCG GCAGGCCCTG CCATAGCCTC AGGTTACTCA
3481  TATATACTTT AGATTGATTT AAAACTTCAT TTTTAATTTA AAAGGATCTA GGTGAAGATC
3541  CTTTTTGATA ATCTCATGAC CAAAATCCCT TAACGTGAGT TTTTCGTTCCA CTGAGCGTCA
3601  GACCCCGTAG AAAAGATCAA AGGATCTTCT TGAGATCCTT TTTTCTGCG CGTAATCTGC
3661  TGCTTGCAAA CAAAAAACC ACCGCTACCA GCGGTGGTTT GTTTGCCGGA TCAAGAGCTA
3721  CCAACTCTTT TTCCGAAGGT AACTGGCTTC AGCAGAGCGC AGATACCAA TACTGTCCTT
3781  CTAGTGTAGC CGTAGTTAGG CCACCACTTC AAGAACTCTG TAGCACCGCC TACATACCTC
3841  GCTCTGCTAA TCCTGTTACC AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG TCTTACCGGG
3901  TTGGACTCAA GACGATAGTT ACCGGATAAG GCGCAGCGGT CGGGCTGAAC GGGGGGTTTCG
3961  TGCACACAGC CCAGCTTGGA GCGAACGACC TACACCGAAC TGAGATACCT ACAGCGTGAG
4021  CTATGAGAAA GCGCCACGCT TCCCGAAGGG AGAAAGGCGG ACAGGTATCC GGTAAGCGGC
4081  AGGGTCGGAA CAGGAGAGCG CACGAGGGAG CTTCCAGGGG GAAACGCCTG GTATCTTTAT
4141  AGTCCTGTCG GGTTTCGCCA CCTCTGACTT GAGCGTCGAT TTTTGTGATG CTCGTCAGGG
4201  GGGCGGAGCC TATGGAAAAA CGCCAGCAAC GCGGCCTTTT TACGGTTCCT GGCCTTTTGC
4261  TGGCCTTTTG CTCACATGTT CTTTCCTGCG TTATCCCCTG ATTCTGTGGA TAACCGTATT
4321  ACCGCC
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Restriction Map of pMEV-2HA

This list contains restriction enzymes cut four times or fewer.

	#sites	-- Bp position of recognition site --			
AatII	4	274,	327,	410,	596
Acc65I	1	935			
AccI	1	947			
AflII	1	828			
AflIII	3	929,	1242,	4274	
Alw44I	1	3960			
AlwNI	2	3452,	3860		
ApoI	4	923,	1069,	1274,	1285
AvaI	2	918,	952		
AvaII	2	2872,	3317		
BamHI	1	903			
BanII	4	725,	1543,	2717,	3427
BbeI	1	2355			
BciVI	4	846,	1774,	2564,	4065
BlnI	2	2178,	3193		
BmrI	3	447,	2062,	2295	
BpmI	2	3154,	3175		
BsaAI	3	491,	1470,	2658	
BsaBI	2	1222,	2211		
BsaI	1	3351			
BsaWI	4	2387,	3231,	3921,	4068
BseRI	1	2159			
BseSI	3	2298,	2391,	3960	
BsiEI	4	661,	958,	2262,	3937
BsiHKAI	4	725,	2465,	2655,	3960
BsmI	2	1039,	1138		
BspHI	2	1782,	3554		
BspMI	3	2252,	2615,	3065	
BsrBI	4	1614,	1778,	2967,	3021
BsrDI	2	66,	2582		
BsrGI	1	96			
BssSI	3	2948,	3074,	4101	
BstAPI	4	796,	1917,	1989,	3451
BstBI	1	3037			
Bsu36I	2	1835,	3467		
BtsI	1	1043			
Cfr10I	4	1573,	2675,	2856,	3139
ClaI	2	1229,	2195		
DraI	3	1183,	3498,	3517	
DraIII	1	1467			
DrdI	4	811,	1421,	2377,	4166
EarI	3	1828,	2705,	2915	
Ecl136II	1	725			
Eco52I	2	958,	2262		
Eco57I	3	2481,	2913,	3747	
EcoO109I	1	3453			
EcoRI	1	923			
EheI	1	2355			
FspI	1	2456			

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HaeII	4	1619,	1627,	2355,	4030
HincII	3	675,	947,	1122	
HindIII	1	756			
HpaI	1	1122			
KasI	1	2355			
KpnI	1	935			
MluI	2	929,	1242		
MscI	3	8,	62,	2436	
MslI	2	514,	2789		
MunI	1	1133			
NaeI	3	1573,	2856,	3139	
NarI	1	2355			
NcoI	4	513,	841,	2085,	2788
NdeI	1	386			
NgoMIV	3	1573,	2856,	3139	
NheI	1	912			
NotI	1	957			
NsiI	2	1924,	1996		
NspI	4	1922,	1994,	2757,	4274
PciI	1	4274			
Ppu10I	2	1924,	1996		
PsiI	2	1102,	1342		
PstI	1	834			
PvuI	1	661			
PvuII	2	1852,	2460		
RsrII	1	2871			
SacI	1	725			
SacII	1	907			
SalI	1	947			
SapI	2	2705,	2915		
SexAI	1	1945			
SfcI	4	834,	1691,	3818,	4009
SfiI	1	2124			
SgfI	1	660			
SmaI	1	952			
SnaBI	1	491			
SpeI	1	152			
SphI	3	1922,	1994,	2757	
SspI	4	3,	50,	1262,	1815
StuI	1	2175			
Tsp45I	3	1646,	2477,	2783	
Tth1111I	1	2471			
VspI	1	159			
XbaI	1	941			
XhoI	1	918			
XmaI	1	952			